



IFWO

RAW SEQUENCE LISTING

DATE: 09/01/2004

PATENT APPLICATION: US/10/828,828

TIME: 12:53:28

Input Set : N:\CrF3\RULE60\10828828.raw

Output Set: N:\CRF4\09012004\J828828.raw

1 <110> APPLICANT: Donoho, Gregroy
 2 Hilbun, Erin
 3 Turner, Alex
 4 Friedrich, Glenn
 5 Zambrowicz, Brian
 6 Sands, Arthur T.
 7 <120> TITLE OF INVENTION: Novel Human Kinase Protein and
 8 Polynucleotides Encoding the Same
 9 <130> FILE REFERENCE: LEX-0119-USA
 10 <140> CURRENT APPLICATION NUMBER: US/10/828,828
 11 <141> CURRENT FILING DATE: 2004-04-21
 12 <150> PRIOR APPLICATION NUMBER: US/09/765,068
 13 <151> PRIOR FILING DATE: 2001-01-18
 14 <150> PRIOR APPLICATION NUMBER: US 60/176,690
 15 <151> PRIOR FILING DATE: 2000-01-18
 16 <160> NUMBER OF SEQ ID NOS: 3
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1269
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
 23 <400> SEQUENCE: 1

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| 24 | atggaccatc ctagtaggga aaaggatgaa agacaacgga caactaaacc catggcacia | 60 |
| 25 | aggagtgcac actgctctcg accatctggc tcctcatcgt cctctggggg tcttatgggtg | 120 |
| 26 | ggacccaact tcagggttgg caagaagata ggatgtggga acttcggaga gctcagatta | 180 |
| 27 | ggtaaaaatc tctacaccaa tgaatatgta gcaatcaaac ttggaaccaat aaaatcacgt | 240 |
| 28 | gctccacagc ttcattttaga gtacagattt tataaacagc ttggcagtg cagggtgaagg | 300 |
| 29 | ctccacacagg tgtattactt tggaccatgt gggaaatata atgccatggt gctggagctc | 360 |
| 30 | cttggcccta gcttggagga cttgtttgac ctctgtgacc gaacatttac tttgaagacg | 420 |
| 31 | gtgttaatga tagccatcca gctgctttct cgaatggaat acgtgcactc aaagaacctc | 480 |
| 32 | atttaccgag atgtcaagcc agagaacttc ctgattgggtc gacaaggcaa taagaaagag | 540 |
| 33 | catgttatac acattataga ctttggactg gccaaaggaat acattgaccc cgaaaccaa | 600 |
| 34 | aaacacatac cttataggga acacaaaagt ttaactggaa ctgcaagata tatgtctatc | 660 |
| 35 | aacacgcac tttggcaaaga gcaaagccgg agagatgatt tgggaagccct aggccatatg | 720 |
| 36 | ttcatgtatt tccttcgagg cagcctcccc tggcaaggac tcaaggctga cacattaaaa | 780 |
| 37 | gagagatata aaaaaattgg tgacaccaa aggaatactc ccattgaagc tctctgtgag | 840 |
| 38 | aactttccag aggagatggc aacctacctt cgatatgtca ggcgactgga cttctttgaa | 900 |
| 39 | aaacctgatt atgagtattt acggaccctc ttcacagacc tctttgaaaa gaaaggctac | 960 |
| 40 | acctttgact atgcctatga ttgggttggg agacctattc ctactccagt aggggtcagtt | 1020 |
| 41 | cacgtagatt ctgggtgcac tgcaataact cgagaaagcc acacacatag ggatcggcca | 1080 |
| 42 | tcacaacagc agcctcttcg aaatcaggtg gttagctcaa ccaatggaga gctgaatggt | 1140 |
| 43 | gatgatccca cgggagccca ctccaatgca ccaatcacag ctcatgccga ggtggaggta | 1200 |
| 44 | gtggaggaag ctaagtgcgt ctgtttcttt aagaggaaaa ggaagaagac tgctcagcgc | 1260 |

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48 <211> LENGTH: 422
49 <212> TYPE: PRT
50 <213> ORGANISM: Homo sapiens
51 <400> SEQUENCE: 2
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53      1          5          10          15
54      Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly Ser Ser
55      20          25          30
56      Ser Ser Ser Gly Val Leu Met Val Gly Pro Asn Phe Arg Val Gly Lys
57      35          40          45
58      Lys Ile Gly Cys Gly Asn Phe Gly Glu Leu Arg Leu Gly Lys Asn Leu
59      50          55          60
60      Tyr Thr Asn Glu Tyr Val Ala Ile Lys Leu Glu Pro Ile Lys Ser Arg
61      65          70          75          80
62      Ala Pro Gln Leu His Leu Glu Tyr Arg Phe Tyr Lys Gln Leu Gly Ser
63      85          90          95
64      Ala Gly Glu Gly Leu Pro Gln Val Tyr Tyr Phe Gly Pro Cys Gly Lys
65      100         105         110
66      Tyr Asn Ala Met Val Leu Glu Leu Leu Gly Pro Ser Leu Glu Asp Leu
67      115         120         125
68      Phe Asp Leu Cys Asp Arg Thr Phe Thr Leu Lys Thr Val Leu Met Ile
69      130         135         140
70      Ala Ile Gln Leu Leu Ser Arg Met Glu Tyr Val His Ser Lys Asn Leu
71      145         150         155         160
72      Ile Tyr Arg Asp Val Lys Pro Glu Asn Phe Leu Ile Gly Arg Gln Gly
73      165         170         175
74      Asn Lys Lys Glu His Val Ile His Ile Ile Asp Phe Gly Leu Ala Lys
75      180         185         190
76      Glu Tyr Ile Asp Pro Glu Thr Lys Lys His Ile Pro Tyr Arg Glu His
77      195         200         205
78      Lys Ser Leu Thr Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr His Leu
79      210         215         220
80      Gly Lys Glu Gln Ser Arg Arg Asp Asp Leu Glu Ala Leu Gly His Met
81      225         230         235         240
82      Phe Met Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu Lys Ala
83      245         250         255
84      Asp Thr Leu Lys Glu Arg Tyr Gln Lys Ile Gly Asp Thr Lys Arg Asn
85      260         265         270
86      Thr Pro Ile Glu Ala Leu Cys Glu Asn Phe Pro Glu Glu Met Ala Thr
87      275         280         285
88      Tyr Leu Arg Tyr Val Arg Arg Leu Asp Phe Phe Glu Lys Pro Asp Tyr
89      290         295         300
90      Glu Tyr Leu Arg Thr Leu Phe Thr Asp Leu Phe Glu Lys Lys Gly Tyr
91      305         310         315         320
92      Thr Phe Asp Tyr Ala Tyr Asp Trp Val Gly Arg Pro Ile Pro Thr Pro
93      325         330         335
94      Val Gly Ser Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu

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1269

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95          340          345          350
96 Ser His Thr His Arg Asp Arg Pro Ser Gln Gln Gln Pro Leu Arg Asn
97          355          360          365
98 Gln Val Val Ser Ser Thr Asn Gly Glu Leu Asn Val Asp Asp Pro Thr
99          370          375          380
100 Gly Ala His Ser Asn Ala Pro Ile Thr Ala His Ala Glu Val Glu Val
101          385          390          395          400
102 Val Glu Glu Ala Lys Cys Cys Cys Phe Phe Lys Arg Lys Arg Lys Lys
103          405          410          415
104 Thr Ala Gln Arg His Lys
105          420
107 <210> SEQ ID NO: 3
108 <211> LENGTH: 1968
109 <212> TYPE: DNA
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111 <400> SEQUENCE: 3
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114 ctgctctcga ccatctggct cctcatcgct ctctgggggt cttatggtgg gaccaactt      180
115 cagggttggc aagaagatag gatgtgggaa cttcggagag ctcagattag gtaaaaatct      240
116 ctacaccaat gaatatgtag caatcaaact ggaaccaata aaatcacgtg ctccacagct      300
117 tcatttagag tacagatttt ataaacagct tggcagtgca ggtgaagggt tcccacaggt      360
118 gtattacttt ggaccatgtg ggaaatataa tgccatgggt ctggagctcc ttggccctag      420
119 cttggaggac ttgtttgacc tctgtgaccg aacatttact ttgaagacgg tgttaatgat      480
120 agccatccag ctgctttctc gaatggaata cgtgcactca aagaacctca tttaccgaga      540
121 tgtcaagcca gagaacttcc tgattggtcg acaaggcaat aagaaagagc atgttatata      600
122 cattatagac tttggactgg ccaaggaata cattgacccc gaaacaaaaa aacacatacc      660
123 ttatagggaa cacaaaagtt taactggaac tgcaagatat atgtctatca acacgcatct      720
124 tggcaaagag caaagccgga gagatgattt ggaagcccta ggccatatgt tcatgtattt      780
125 ccttcgaggc agcctccctt ggcaaggact caaggtgac acattaaaag agagatatca      840
126 aaaaattggt gacacaaaaa ggaatactcc cattgaagct ctctgtgaga actttccaga      900
127 ggagatggca acctaccttc gatatgtcag gcgactggac ttctttgaaa aacctgatta      960
128 tgagtattta cggacctctc tcacagacct ctttgaaaag aaaggctaca cctttgacta      1020
129 tgcctatgat tgggttggga gacctattcc tactccagta gggtcagttc acgtagattc      1080
130 tgggtgcatc gcaataactc gagaaagcca cacacatagg gatcggccat cacaacagca      1140
131 gcctcttcga aatcaggtgg tttagctcaac caatggagag ctgaatgttg atgatccac      1200
132 gggagcccac tccaatgcac caatcacagc tcatgccgag gtggaggtag tggaggaagc      1260
133 taagtgtctg tgtttcttta agaggaaaag gaagaagact gctcagcgcc acaagtgacc      1320
134 agtgccctcc aggagtcctc aggccctggg gactctgact caattgtacc tgcagctcct      1380
135 gccatttctc attggaaggg actcctcttt gggggagggt ggatatccaa accaaaaaga      1440
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137 ccctctccgc ctgcctaagg ctctgagcag gtcccagagc tgctgttcct ccactgcttg      1560
138 cccatagggc tgccctggtg actctccttc ccattgttta cagtgaagggt gtcattcaca      1620
139 aaaactcaag gactgctatt ctccctcttc cccttagttt actcctggtt tttaccccac      1680
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143 gcagattca tcccagctgg cccttgaggt tcaggttcct tcttccctcc ctccgtgtgaa      1920
144 gttacactgt aggacacaag ctgtgagcaa tctgcagttc actggccc      1968

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VERIFICATION SUMMARY

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